

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2003, 15:23:30 ; Search time 467 Seconds

(without alignments)
4375.749 Million cell updates/sec

Title: US-09-494-297-2

Perfect score: 3945
Sequence: 1 MKTRPNNLNTLNTORVLS.....IAGISIGINGTIRIRKRD 757

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL-frame+ .p2n .model -DEV-xlp
-O/-cgn2_1/USPTO.spool/US09494297/rnat_13082003_122946_28082/app_query.fasta_1.903
-DB-N-geneseq_19Jun03 -OPMT-fastap -SUFFIX-rng -MINMATCH-0.1 -LOOPT-0
-LOOPT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosom62 -TRANS-human0.cdl
-LIST-45 -DOCALLING-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-p2n -NORM-ext -HEAPSIZ-500 -MINLEN-0 -MAXLEN-2000000000
-USBR-US09494297.ecgn_1.1.304 -runat_13082003_122946_28082 -NCP-6 -ICP-3
-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -MAIT -DSPELOCK-100 -LONELOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREDS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7

Database : N.Geneseq_19Jun03:*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
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16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
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20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3945	100.0	2286	24	ABN69678
2	236.5	6.0	1020	24	ABN69681
3	196	5.0	15614	20	AA12982
4	196	5.0	15614	24	ABN98777
5	180	4.6	2127	21	AAA30874
6	178	4.5	7650	20	AAV82019
7	177	4.5	49617	22	AAV82541
8	176	4.5	2718	20	AAV82021
9	161	4.1	4161	24	ABQ69442
10	161	4.1	4185	24	ABQ67871
11	161	4.1	4249	20	AA120201
12	161	4.1	4249	24	ABN98186
13	161	4.1	4249	25	ABX61756
14	161	4.1	4359	24	ABN98185
15	161	4.1	4359	25	ABX61755
16	161	4.1	12445	20	AA13179
17	161	4.1	12445	24	ABN98974
18	161	4.1	1163020	24	ABQ67197
19	161	4.1	3011208	24	ABQ69245
20	161	4.0	4593	24	ABQ68111
21	159	4.0	4593	24	ABQ70032
22	159	4.0	2944528	24	ABA03041
23	159	4.0	4557	24	ABK75341
24	156	3.9	2499	24	ABQ68254
25	155	3.9	2499	24	ABQ68254
26	155	3.9	2499	24	ABQ68254
27	155	3.9	2944528	24	ABA03041
28	154	3.9	5547	18	AAV68844
29	152.5	3.9	6042	19	ABQ69231
30	152	3.9	7551	18	AAV68843
31	152	3.9	7551	18	AAV68843
32	152	3.9	7551	18	AAV68843
33	152	3.9	7551	18	AAV68843
34	152	3.9	7551	18	AAV68843
35	152	3.9	7551	18	AAV68843
36	152	3.9	7551	18	AAV68843
37	152	3.9	7551	18	AAV68843
38	150	3.8	3698	24	ABD35550
39	149	3.8	2700	21	AAV97541
40	149	3.8	3945	20	AAV7593
41	149	3.8	4143	25	ABT14918
42	149	3.8	6168	20	AAV20228
43	149	3.8	6168	20	AAV20230
44	149	3.8	6168	20	AAV20232
45	149	3.8	6168	24	ABN98213

ALIGNMENTS

RESULT 1
ABN69678
ID ABN69678 standard; DNA; 2286 BP.
XX
XX ABN69678;
XX
XX 01-JUL-2002 (first entry)
XX
XX Streptococcus polynucleotide SEQ ID NO 7269.
XX
XX
XX Streptococcus: GAS; GBS; group B streptococcus; Streptococcus agalactiae;
XX Streptococcus: Streptococcus pyogenes; antibacterial; gene;
XX anti-inflammatory; Infection; vaccine; meningitis; gene therapy; ds.
XX Streptococcus pyogenes.
XX
XX WO200234771-A2.
PN

QY 461 ArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLys 480
DB 1396 CGTACCTCTTTAAATATACGTGAACCAAGACATACCATCTGACACCTTTCTTAAA 1455
QY 481 HistLeuLysValLleGluLysGlyTyrArgGluLysGlyGlnAlaLleGlyTyrSer 500
DB 1456 CATATCAAAAAGAAATGAGAAAGGTTACAGGAAAGCAAGCAAGCTAATGAGATATGT 1515
QY 501 GlyLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaLleTyrTyrPheThrAsp 520
DB 1516 GGCTACTAGACACATTCGCGGCTACTACAGTACGCAATATATATTCACATGAT 1575
QY 521 SerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAsp 540
DB 1576 AGTCCTGAATTAAGATTAAGATAAAGTAAAGACATCATGTTTGAGACATGAAATGAT 1635
QY 541 SerThrLeuAlaAlaAlaLysLleLeuValGluTyrAlaGlnAspSerAsnProProGln 560
DB 1636 AGTACTTACAGTGTGCTAAATCCCTGTGAAATACCTCAAGATATATCCCTCCACAG 1695
QY 561 LeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuLleGlyTyr 580
DB 1696 CTAACTGACCTGATTTCTTTATCCGAATACATATATATATCTTATTTGAACT 1755
QY 581 GlnThrHisProGluAspLeuValAspLleIleArgMetGluAspLysGluValLle 600
DB 1756 CAGTGGCATCCAGAAATTTAGTTGATATATTCGATGAGACATTAAGAAAGATTTATN 1815
QY 601 ProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspParGthr 620
DB 1816 CCGTATACATATATATTAACATTCGAGAAACCGTACCTGTTACTGCTGACACAACT 1875
QY 621 LysAspPheHisPheGluLleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThr 640
DB 1876 AAAGATTTCCATTTGAAATTTGAATTAATAAATAATACGAAATTCCTTTCTCAACT 1935
QY 641 ValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLys 660
DB 1936 GTTAAACAGATTAACCAACCTCGAATTTAAAGATGTTAAACCAACCTATATTTAAAA 1995
QY 661 HisGlyLysSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGlu 680
DB 1996 CAGGGGAAAGTTAACTTCAAGGTTTACCGAAGGTTATCTTACCTGCAAGAA 2055
QY 681 ThrAspSerGluLysTyrLysValLysValAsnSerGlnGluValAlaAsnAlaThrVal 700
DB 2056 ACAGATTCGAAGGCTATAGTTAAAGTTAATAGCCAGAAAGTACCAATGCTACAGTT 2115
QY 701 SerLysThrGlyLleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProVal 720
DB 2116 TCATAAACAAGAAATTAACAAGTATGACACTTGTGAAATAATTAAGAGCCTGTT 2175
QY 721 ValProThrGlyValAspGlnLysLleAsnGlyTyrLeuAlaLeuLleValLleAlaGly 740
DB 2176 GTTCCACAGAGAGTTCATCAAAAGATCAATGCTATCTGCTTGTAGTTATTCGCTGT 2235
QY 741 HisSerLeuGlyLleThrPglyLleHisThrIleArgLysHisAsp 757
DB 2236 ATCAGTTTGGGATCGGGGAATTCACAGATTAAGATTAAGAAACATGAC 2286

RESULT 2
ABN69681 standard. DNA: 1020 BP.

AC ABN69681;
DE 01-JUL-2002 (first entry)
XX Streptococcus polynucleotide SEQ ID NO 7275.
KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
group A streptococcus; Streptococcus pyogenes; antibacterial; gene;
antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

XX OS Streptococcus pyogenes.
XX PN WO200234771-A2.
XX PD 02-MAY-2002.
XX PF 29-OCT-2001; 2001WO-GB04789.
XX PR 27-OCT-2000; 2000GB-0026333.
XX PR 24-NOV-2000; 2000GB-0028727.
XX PR 07-MAR-2001; 2001GB-0005640.
XX PA (CHIR-) CHIRON SPA.
XX PI (GENO-) INST GENOMIC RES.
XX PI Telford J, Maignan V, Margalit Ros YI, Grandi G, Fraser C;
XX Tettelin H;
XX WPI; 2002-352536/38.
XX DR P-PSDB; ABP29050.
XX PT New Streptococcus protein for the treatment or prevention of infection
XX PT or disease caused by Streptococcus bacteria, such as meningitis, and
XX PT for detecting a compound that binds to the protein.
XX PS Claim 7; Page 3880; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC used as a vaccine or diagnostic composition. The disease caused by
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins.
XX SQ Sequence 1020 BP; 375 A; 162 C; 196 G; 287 T; 0 other;
Alignment Scores:
Pred. No.: 1,83e-09 Length: 1020.
Score: 236.50 Matches: 96
Percent Similarity: 40.43% Conservative: 54
Best Local Similarity: 25.88% Mismatches: 118
Query Match: 5.99% Indels: 103
DB: 24 Gaps: 16
US-09-494-297-2 (1-757) x ABN69681 (1-1020)
QY 404 ThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsn-----GlySerSer 421
DB 73 ACTGTTGTAATACGAGCAACTAACACTTCAAAAACCTGATTTGTTAATAGCAAT 132
QY 422 GlnValValTyrCysPheAsnAlaAspLeuLysSerProProAsp-----SerGlu 438
DB 133 GCATTAAATCCAAATACAGATTTCATTTAAATTCGAACCTGATACTACTGTCACAGAA 192
QY 439 AspGlyGlyLysThrMetThrProAspPheThrGlyGluValLysTyrThrHisLle 458
DB 193 GACGGAATTAAGTTAAAGGTGTGCTTGAACACCCGATGACTAAAGTCACCTTAC--- 249
QY 459 AlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPhe 478
DB 250 -----ACCAATTCAGAT----- 261